Í

KCCB\_RAT KCCB\_WAN CDPK\_SOYBN CSKP\_MOUSE CDP2\_MAIZE CSKP\_HUMAN KPBH\_RAT KPBH\_HUMAN KCC1\_SCHPO KPBH\_MOUSE KIIO\_ARATH

P08413 rattus norv
Q13554 homo sapien
P28583 glycine max
O70589 mus musculu
P49101 zea mays (m
Q62915 rattus norv
Q14936 homo sapien
P31328 rattus norv
P15735 homo sapien
Q99712 schizosacch
Q9db30 mus musculu
Q38997 arabidopsis

ALIGNMENTS

```
Post-processing: Minimum Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seg length: 0 seg length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query
           BLOSUM62
Gapop 10.0 ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       May 18, 2002, 04:48:39; Search time 42.56 Seconds (without alignments) 327.515 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SwissProt_40:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105224 seqs,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-719-748-2
1846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEPFKQQKVEDFYDIGEELG.....TEEDIARRKALHPRRRSSTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length DB
           GenCore version (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38719550 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08
        CDP3_ORYSA
DCK1_HUMAN
KCCA_RAT
DCK1_MOUSE
DCK1_RAT
CCDP1_ORYSA
KCCA_MOUSE
KCCB_MOUSE
CDPK_DAUCA
                                                                                                                                             KMLS_SHEEP
KMLC_RAT
KMLC_DICDI
KCC4_RAT
KCC1_HUMAN
KCC1_RAT
KCC4_HUMAN
KCC1_HUMAN
KCC4_MOUSE
KCC4_MOUSE
KCC4_MOUSE
KCC4_RAT
TRIO_HUMAN
KCC6_RAT
TRIO_HUMAN
KCC6_RAT
TRIO_HUMAN
CDP1_ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                              KMLS_CHICK
S17A_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                             KMLS_HUMAN
KMLS_RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DAPK_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                              S17B_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                              S17A_RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 4.5
Compugen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105224
                                    P29294
P11799
Q9uene
Q9uene
Q9uene
Q9uene
Q9uene
Q9uene
Q143234
P13234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q28824
Q15746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P53355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
                      mus musculu
rattus norv
oryza sativ
mus musculu
mus musculu
                                                                                                                                                           homo sapien
rattus norv
homo sapien
oryza sativ
                                                                                                                                                                                                                        homo sapien
homo sapien
mus musculu
rattus norv
                                                                                                                                                                                                                                                                                                                                                                                ovis
                                                                                                                                                                                                                                                                                                                                   rattus norv
dictyosteli
                                                                                                                                                                                                                                                                                                                                                                                                            homo sapien 
oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                           oryctolagus
gallus gall
                                                                                                                  homo sapien
                                                                                                                              arabidopsis
oryza sativ
                                                                                                                                                                                                                                                                                      homo sapien
rattus norv
                                                                                                                                                                                                                                                                                                                    rattus norv
                                                                                                                                                                                                                                                                                                                                                                 oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          homo sapien
                                                                                                                                                                                                                                                                                                                                                                              sapien
aries
RESULT 1

DAPK_HUMAN STANDARD; PRT; 1431 AA.

AC DAPK_HUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               335
335
337
337
339
344
344
344
354
                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                 -!-:PTM: AUTOPHOSPHORYLATED.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES
-!- SIMILARITY: CONTAINS 10 ANK REPEATS.
-!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REVISIONS TO 164-171.

REVISIONS TO 164-171.

REINSTEIN E.;

Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: INVOLVED IN MEDIATING INTERFERON-GAMMA-INDUCED CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             478
477.5
476.5
476.5
475.5
475.5
473.5
473.5
473.5
473.5
473.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             542
508
508
513
513
513
406
406
512
```

15-kD

Result

Score

33233118 33233118 33233118 33233118

70393 70393 70393 6986 6685 6685 6640 66595 6640 605 605 605 532 530.5 500.5 500.5 500.5 500.5 500.5 500.5 500.5 500.5 500.5 500.5 5

486 485.5 482.5

486.5

Minimum DB

Scoring table: Sequence: Perfect score: Run on:

Database

```
Ş
                                                                                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                              Ş
                                                                                                                                                                                                                                               QΥ
                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                 Ş
                                                                                                                                                                                                     ₽
                                                                                                                                                                                                                   δã
                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 242
                                                                                                                                                                                                                                                                                                                                                                                                        Transferase; Serit
Phosphorylation; P
DOMAIN 267
SEPEAT 411
REPEAT 411
REPEAT 411
REPEAT 511
REPEAT 511
REPEAT 577
REPEAT 610
REPEAT 610
REPEAT 610
REPEAT 610
REPEAT 1153
DOMAIN 1153
DOMAIN 1313
NP_BIND 19
BINDING 42
ACT_SITE 139
MUTAGEN 42
SEQUENCE 1431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                              Eukaryota; Metazoa; (
Mammalia; Eutheria; (
Bovidae; Bovinae; Bos NCBI_TaxID=9913;
                                                                                                                                       BOVIN
                                                                              RMLS_BOVIN STANDARD; PRT; 1176 AA (228824); Created)
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat Myosin 119th chain kinase, smooth muscle (E (Contains: Telokin).
                                                               Bos taurus
                                                                         MYLK.
                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                     121
TISSUE-Stomach;
MEDLINE-93203148;
                                                                                                                                                                                                                                                     181
                                                                                                                                                                                                      241
                                                                                                                                                                        301
                                                                                                                                                                                      301
                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                    61
                 EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                  KQILDGVNYLHTKKIAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGT
                                                                                                                                                                                VRRRWKLSFSIVSLCNHLTRSLMKKVHL---RPDEDLRNCESDTEEDIARRKALH
                                                                                                                                                                                                              FSHTSELAKDFTRKLLVKETRKRLTIQEALRHPWITPVDNQQAMVRRESVVNLENFRKQY
                                                                                                                                                                                                                                                                     FSNTSALAKDF IRRLLVKDPKKRMT IQDSLQHPWIKPKDTQQALSRKASAVNMEKFKKFA
                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS00107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS00108
                                                               (Bovine).
                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; PROTEIN_KINASE_ST; 1.
ine/threonine-protein kinase; Calmodulin-binding;
ATP-binding; Repeat; ANK repeat; Apoptosis.
PROTEIN KINASE.
334 CALMODULIN-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                           ΑĄ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN_KINASE_DOM;
PROTEIN_KINASE_ST;
                                                                                                                                                                                                                                                                                                                                                                                                                         266
334
440
440
473
507
573
606
639
906
1197
1397
1397
                                          Bos.
  PubMed=1284247
                                                                                                                                                                                                                                                                                                                                                                            70.0%;
                                                 Cetartiodactyla; Ruminantia;
                                                           Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                            160017
                                                                                                                                                                                                                                                                                                                                                                                                       ANK 1.

ANK 2.

ANK 3.

ANK 4.

ANK 5.

ANK 6.

ANK 7.

ANK 10.

DEATH.

ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY).

BY SIMILARITY).

BY SIMILARITY).

BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                     62;
                                                                                                                                                                                                                                                                                                                                                                           Score 1293; DB 1;
Pred. No. 4.3e-71;
                                                          Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY.
>A: LOSS OF ACTIVITY.
9EE84811004A155B CRC64;
                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.
                                                                                          update)
                                                                                                                                                                                                                                                                                                                                                                      43;
                                                                                           2.7.1.117) (MLCK)
                                                                                                                                                                          -DEEDSFVMKAIIH
                                                                                                                                                                                                                                                                                                                                                                                     Length 1431;
                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                           Euteleostomi;
                                                     Bovoidea
                                                                                                                                                                                                                                                                                                                                                                       8;
                                                                                                                                                                            350
                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                         120
                                                                                                                                                                                                                                                                                                                                                        60
                                                                                                                                                                                                                                                                                                          120
                                                                                                                                                                                                                                                                                                                                         60
                                                                                                                                                                                                                           300
                                                                                                                                                                                                                                                                                          180
                                                                                                                                                                                                                                           240
                                                                                                                                                                                                                                                          240
                                                                                                                                                                                                                                                                          180
                                                                                                                                                                                                                                                                                                                                                                        Ν
```

Í

```
THE TREE TO SEE THE TREE TO SEE THE TREE TO SEE THE TREE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00047; 19; 2.

Pfam; PF00069; pkinase; 1.

SMART; SM00060; FN3; 1.

SMART; SM00410; IG_1ike; 1.

SMART; SM00408; IGC2; 2.

SMART; SM00220; S_TKC; 1.

SMART; SM00220; PROTEIN_KII

PROSITE; PS00107; PROTEIN_KII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kobayashi H.,
Ebashi S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is not as long as long as its content is not as long as l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
INIT_MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; S57131; AAB25794.1; HSSP; P56276; 1TLK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transferase; Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                         REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [nterPro;
                           REPEAT
REPEAT
DOMAIN
DOMAIN
                                                                                                                             REPEAT
REPEAT
                                                                                                                                                                                                            REPEAT
REPEAT
                                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                                       REPEAT
                                                                                                                                                                                 REPEAT
                                                                                                                                                                                                                                                                                                                                                                     REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11ght-chain] phosphate.
SUBUNIT: TELOKIN BINDS CALMODULIN.
SUBUNIT: TELOKIN BINDS CALMODULIN.
ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS OF MLCK ARE PRODUCED FAITERNATIVE INITIATION, A NON-MUSCLE FORM (WHICH IS THE LONGEST ALTERNATIVE INITIATION, A NON-MUSCLE FORM (WICH IS THE LONGEST ORM); A SMOOTH-MUSCLE FORM AND TELOKIN (A C-TERMINAL SECTION WINO CATALYTIC ACTIVITY).
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR003598; Ig_c2.
IPR003600; Ig_like.
IPR002290; Ser_thr_pkinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR000719; Euk_pkinase.
IPR003961; FN_III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR003006; Ig_MHC. IPR003598; Ig_c2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           initiation
        124
1136
1148
1160
1172
1196
208
2208
232
232
244
256
268
268
268
268
268
268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inoue A.,
     1176
1022
1291
111
111
123
123
135
147
147
1159
1171
183
195
207
219
223
243
243
243
255
267
279
279
279
279
280
290
1035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         institutions as long as its content is in no way attement is not removed. Usage by and for commercial license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mikawa T., Kuwayama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELOKIN.
FOR TELC
16 x 12
                                                                                       5.
6.
7.
10.
11.
11.
11.
11.
11.
11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MYOSIN LIGHT
        FIBRONECTIN TYPE-III.
PROTEIN KINASE.
CALMODULIN-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISOZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                         (INCOMPLETE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R TELOKIN.
X 12 AA TANDEM REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Η.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Calmodulin-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hotta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OF A SPECIFIC SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KINASE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ۲.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMOOTH-MUSCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Masaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [myosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SERINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ή.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HIIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВΥ
```

```
RESULTING TO SEE THE RESULT OF SEE THE RESULT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SO FT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local (
                                                                                                                                                                             REVISIONS.
Birukov K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
NP_BIND
BINDING
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1998 (Rel. 36, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Myosin light chain kinase, smooth muscle and non-muscle (EC 2.7.1.117) (MLCK) [Contains: Telokin (Kinase related
MEDLINE=99216419; PubMed=10198165;
Lazar V.L., Garcia J.G.N.;
"A single human myosin light chain
Genomics 57:256-267(1999).
                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 1).
TISSUE-Umbilical vein endothelial cells;
MEDLINE-97304466; PubMed-9160829;
Garcia J.G.N., Lazar V.L., Gilbert-Mccla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q15746; Q14844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9UIT9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                        TISSUE-Umbilical vein
                                                                                                           SEQUENCE FROM N.A. (ISOFORMS
                                                                                                                                                        Submitted
                                                                                                                                                                                                                                                                 regulation
                                                                                                                                                                                                                                                                                   "Myosin light
                                                                                                                                                                                                                                                                                                          Verin A.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MYLK OR MLCK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KWQKTGNAVRAIGRLSSMAMISGLSGRKSSTGSPTSPL-NAEKLESEDVSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RWKLSFSIVSLCNHLTRSLM-----KKVHLRPDEDLRNCESDTEEDIAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SELAKDFIRKLLVKETRKRLTIQEALRHPWI-TPVDNQQAMVRRESVVNLENFRKQYVRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APEIVNYEPLGLEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSYDFDEEFFSHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DGVNYLHTKKTAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGTPEFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMNCLHHPKLVQCVDAFEEKANIVMVLEIVSGGELFERIIDEDFELTERECIKYMKQIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EQKVSDFYDIEERLGSGKFGQVFRLVEKKTGKIWAGKFFKAYSAK-----EKENIRQEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SDDAKDFISNLLKKDMKNRLNCTQCLQHPWLMKDTKNMEA----KKLSKDRMKKYMARR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGVEYIHKQGIVHLDLKPENIMCVNKT--GTRIKLIDFGLARRLENAGSLKVLFGTPEFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SILRQVLHHNVITLHDVYENRTDVVHILELVSGGELFDFLAQKE-SLSEEEATSFIKQIL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149;
                                                                                                                                                                                                                                             Respir.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                      .G., Garcia
(MAR-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                   chain kinase in endothelium: molecular cloning
                                                                                                                                                                                                                                             Cell Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD; PI
; Q16794; 095796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1176
AA; 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1151
739
754
846
                                                                                                                                                    J.G.N.;
to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128824
                                                                                                                                                                                                                                          Biol. 16:489-494(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62;
                                                                                                                                                                                                                                                                                                                            Gilbert-Mcclain L.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IG-LIKE C2-TYPE DOMAIN.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ΜW.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 703.5; DB 1
Pred. No. 1.8e-35;
2; Mismatches 117
                      chain kinase
                                                                                                           2
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata;
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RT; 1914 AA.
095797; 095798; 095799;
                                                                                                           3A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F53DC6D4D42D4B97 CRC64;
                                                                                                             3B
                      gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>'</u>1;
                      (MLCK; MYLK).";
                                                                                                                                                                                                                                                                                                                            Gallagher P.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     isozymes
d protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9UBG5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23;
                                                                                                                                                                                                                                                                                   and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7;
```

```
EMBL; U48959; AAC18423.2; ---
EMBL; AF069601; AAD15921.2; --
EMBL; AF069602; AAD15922.1; --
EMBL; AF069603; AAD15923.1; --
EMBL; AF069604; AAD15924.1; --
EMBL; AF069671; AAD51380.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Watterson D.M., Schavocky J.P., Guo L., Weis Shrinsky V.P., Van Eldik L.J., Haiech J.; "Analysis of the kinase-related protein gene 3q21 in a multi-gene cluster: organization, splicing and polymorphic marker."; J. Cell. Biochem. 75:481-491(1999).
                                                                                                               use by non-profit institutions as long a
modified and this statement is not removed.
entitles requires a license agreement (See l
or send an email to license@isb-sib.ch).
                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                    + +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Lung, and Placenta;
MEDLINE=20007838; PubMed=10536370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Hippocampus; MEDLINE-96121365; P
                                                                                                                                                                                                                                                                                                                                                                  -
                                                                                                                                                                                                                                                                                                                                                                                           -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1456-1914 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1614-1914 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Potier M.-C., Chelot Turnell W.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>6</u>
                                                                                                                                                                                                                             ALTERNATIVE PRODUCTS: AT LEAST 6 ISOFORMS; 1 (SHOWN HERE), 2, 3A, 3B, 4 AND DEL-1790; ARE PRODUCED BY ALTERNATIVE SPLICING.

3B, 4 AND DEL-1790; ARE PRODUCED BY ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES ARE EXPRESSED IN A WIDE VARIETY OF ADULT AND FETAL TISSUES AND IN CULTURED ENDOTHELIUM WITH QUALITATIVE EXPRESSION APPEARING TO BE NEITHER TISSUE- NOR DEVELOPMENT-SPECIFIC. NON-MUSCLE ISOFORM 2 IS THE DOMINANT SPLICE VARIANT EXPRESSED IN VARIOUS TISSUES. TELOKIN HAS BEEN FOUND IN A WIDE VARIETY OF ADULT AND FETAL TISSUES. PTM: MLCK IS PROBABLY DOWN-REGULATED BY PHOSPHORYLATION.

SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

SIMILARITY: CONTAINS 1 INMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.

SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                   light-chain] phosphate.
SUBUNIT: TELOKIN BINDS CALMODULIN.
SUBUNIT: TELOKIN BINDS CALMODULIN.
ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS; A NON-MUSCLE FORM
LONGEST FORM), A SMOOTH-MUSCLE FORM AND TELOKIN (A C-TERMINAL
SECTION WITH NO CATALYTIC ACTIVITY); ARE PRODUCED BY ALTERNAT
                                                                                                                                                                                                                                                                                                                                                                                                            INITIATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequencing, expre 29:562-570(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OF 923-1914 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .G., Garcia J.G.N.; (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TO ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=8575746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pekarsky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ۲.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MLCK) from l
localization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gardiner
                                                                                                                                                         There are no restrictions ong as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene found at human chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Weiss C.,
                                                                                                                              http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from hippocampus:
                                                                                                                                               Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ×.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chlenski A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ៥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rossier J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3qcen-q21.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alternative
                                                                                                                                                                                       EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                         ALTERNATIVE
                                                                                                                                                                                          a collaboration -
MBL outstation -
                                                                                                                                               for
                                                                                                                                                                                                                                                                                                        TELOKIN
                                                                                                                                                                                       outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (THE
                                                                                                                                                              00
```

```
R Interry, A.....

R Ffam; PP00047; ig; 8.

P Ffam; PP00047; ig; 8.

P Ffam; PP00047; ig; 8.

P Ffam; PP00069; pkinase; 1.

P Ffam; PP00069; pkinase; 1.

DR SMART; SM00060; FN3; 1.

DR SMART; SM00410; IG_like; 1.

DR SMART; SM00220; S_TKC; 1.

DR SMART; SM00220; S_TKC; 1.

DR PROSITE; PS00110; PROTEIN_KINASE_ST; 1.

DR PROSITE; PS00110; PROTEIN_KINASE_ST; 1.

DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.

W Transferase; Serine/threonine-protein kinase; Calmodulin-binding; KW ATP-binding; Phosphorylation; Alternative splicing.

KW Alternative initiation; Alternative splicing.

KW Alternative initiation; Alternative splicing.

MYOSIN LIGHT CHAIN KINASE, NON-MUSCLE TOWNER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
EMBL;
HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
InterPro;
                                                                                                               DOMAIN
NP_BIND
BINDING
BINDING
BOMAIN
REPEAT
                                                                                                                                                                                                                                                                                                     INIT_MET
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIM;
                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
VARSPLIC
VARSPLIC
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                          INIT_MET
                                                    VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;; AF096766; AAD51380.1; J

; AF096776; AAD51380.1; J

; AF096776; AAD51380.1; J

; AF096770; AAD51380.1; J

; AF096777; AAD51380.1; J

; AF096771; AAD51381.1; J

; AF096771; AAD51381.1; J

; AF096770; AAD51381.1; J

; AF096770; AAD51381.1; J

; AF096770; AAD51381.1; J

; AF096769; AAD51381.1; J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             600922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR000719; Euk_pkinase.
IPR003961; FN_III.
IPR003962; FnIII_repeat.
IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR003600;
IPR002290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR003598;
                                                                                                                                                                                                            1585
1906
868
868
896
924
                                                                                                                                                                                                                                                                                             1761
1343
1464
1711
1824
                                                                                                                                                                                                                                                                                                                                                           1761
923
                                                                         1433
                                                                                                       952
980
999
999
1004
1016
1028
1040
1052
  1655
1790
933
                                                     1473
                                                                                                                                                                                                                                                                                                                                                                                          923
                                                                                                                                                                                                                                                                                                                                                           1914
923
                                                                                                                                                                                                                                                                                                                                                                                          1914
                                                                                                        1891
1493
1585
1585
1914
998
998
923
923
923
979
979
979
979
1003
1015
1015
1027
1027
1039
11039
  1705
1790
933
                                                     1546
                                                                         1439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig_like.
Ser_thr_pkinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOINED.
JOINED.
JOINED.
JOINED.
JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOINED
JOINED
 (IN ISOFORM 4).
MISSING (IN ISOFORM 3
MISSING (IN ISOFORM D
V -> M (IN REF. 5).
                                                                                                                                                                                                                                                                            IG-LIKE
ATP (BY
ATP (BY
                                                                                                                                                                                                                                                                                                                                                ISOZYME.
MYOSIN LIGHT CHAIN KINASE, SMOOTH-MUSCLE
ISOZYME.
TELOKIN.
FOR MYOSIN LIGHT CHAIN KINASE, SMOOTH-
RUSCLE ISOZYME.
                                                                                                                   6 x 1
II-1
II-2.
II-3.
II-4.
II-5.
                                                                                                                                                                                                                                                                                                           CALMODULIN-BINDING
                                                                                                                                                                                                                                                                                                                     PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                             FIBRONECTIN TYPE-III
                                        DEVEYSD -> MKWRCQT (IN ISOFORM 3A,
ISOFORM 3B AND ISOFORM 4).
GKFGQVFRLVEKKTRKVWAGKEFKAYSAKEKENIRQEISIM
NCLHHEKLVQCVDAFEEKANIVMVLEIVSGGEL -> L
                                                                                 VSGIPKPEVAWFLEGTPVRRQEGSIEVYEDAGSHYLCLLKA RTRDSGTYSCTASNAQGQVSCSWTLQVER -> G (IN ISOFORM 2 AND ISOFORM 3B).
                                                                                                                                                                                                                                                                                                                                        FOR TELOKIN
                                                                                                                                                                                                                                                                SIMILARITY.
                                                                                                                                                                   (INCOMPLETE).

12 AA APPROXIMATE TANDEM REPEATS
2 (INCOMPLETE).
                                                                                                                                                                                                                                              28
                                                                                                                                                                                                                                                                          (BY SIMILARITY).

(BY SIMILARITY).
                                                                                                                                                                                                                                              AA APPROXIMATE TANDEM REPEATS
               DEL-1790).
                        3A AND ISOFORM
                          3B).
```

```
밁
                                                                                                                                                                                                                                                                                                                         Š
                                                                                                                                                                                                                                                                                                                                          B
                                                                                                                                                                                                                                                                                                                                                         Ş
                                                                                                                                                                                                                                                                                                                                                                                        8
δÃ
                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                        Qy
                                                                                                                                                                                                                                                                                                          B
                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 14
                                                                                                                KMLS_RABIT STANDARD; PRT;
P29294; Q28729;
01-DEC-1992 (Rel. 24, Created)
15-JUL-1998 (Rel. 36, Last sequence
16-CCT-2001 (Rel. 40, Last annotatic
Myosin light chain kinase, smooth mu
[Contains: Telokin].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                                                           1457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                           1511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
       TISSUE-Smooth muscle;
MEDLINE-92084694; PubMed-1748666;
Gallagher P.J., Herring B.P., Griffin S.A.,
"Molecular characterization of a mammalian
chain kinase.";
J. Biol. Chem. 266:23936-23944(1991).
                                                                                                                                                                                                           1744
                                                                                                                                                                                                                                           1689
                                                                                                                                                                                                                                                                           1629
                                                                                                                                                                          RABIT
                                                                                Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolag
                                                                                                                                                                                                                                                                                                          1571
                                                        SEQUENCE FROM N.A.
                                                                         NCBI_TaxID=9986;
                                                                                                          MYLK.
                                                                                                                                                                                                                                                           245
                                                                                                                                                                                                                                                                                           185
                                                                                                                                                                                                                                                                                                                          125
                                                                                                                                                                                                                           304
                                                                                                                                                                                                                                                                                                                                                           66
                                                                                                                                                                                                                                                                                                                                                                                         6
                                                                                                                                                                                                                                                                                                                                         EQKVSDFYDIEERLGSGKFGQVFRLVEKKTRKVWAGKFFKAYSAK-----EKENIRQEI 1510
                                                                                                                                                                                                                                                                          APEVINYEPIGYATDMWSIGVICYILVSGLSPFMGDNDNETLANVTSATWDFDDEAFDEI
                                                                                                                                                                                                                                                                                                                  DGVNYLHTKKIAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGTPEFV 184
                                                                                                                                                                                                                                                                                                                                                                                         QQKYEDFYDIGEELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVSREEIEREV
                                                                                                                                                                                                                          RWKLSFSIVSLCNHLTRSLM-----KKVHLRPDEDLRNCESDTEEDIAR
                                                                                                                                                                                                                                                                                   APEIVNYEPLGLEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSYDFDEEFFSHT
                                                                                                                                                                                                                                                                                                          KWQKTGNAVRAIGRLSSMAMISGLSGRKSSTGSPTSPLNAEKLESEEDVSQ
                                                                                                                                                                                                                                          SELAKDFIRKLLVKETRKRLTIQEALRHPWI-TPVDNQQAMVRRESVVNLENFRKQYVRR
                                                                                                                                                                                                                                                                                                                                                                                                           al Similarity
146; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                           1563
1609
1639
1639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1300
1316
1326
1478
1511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1210
1280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          963
1022
1048
1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1284
                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            1563
1609
1639
1640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1300
1316
1326
1478
1511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1210
1280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   963
1022
1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1162
                                                                                                                                                                                                                                                                                                                                                                                                                    37
41
                                                                                                                                                                                                                                                                                                                                                                                                                    6.8
                                                                                                                                                                                                                                                                                                                                                                                                             66;
                                                                                                                                    sequence update) annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD15923).

M -> I (IN REF. 3)

AAD15924).

A -> G (IN REF. 5)

T -> S (IN REF. 5)

T -> S (IN REF. 5)

Y -> C (IN REF. 5)

S -> T (IN REF. 5)

A -> P (IN REF. 5)

A -> P (IN REF. 5)

GY -> D (IN REF. 5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S ->
P ->
KPM .
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 698; DB 1;
Pred. No. 6.7e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAD15923
                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ₽P
                                                                                                                             muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (IN
EAH
(IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , in
                                                                                                                                                                     1147
                                                                                                                             update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                             REF. 5).
REF. 5).
REF. 5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REF.
                                   Α.,
                                                                                                                                                                      B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . REF.
                            , Stull smooth
                                                                                     Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     \omega 5 5 5 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ω
••
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ω<u>υ</u>
                                                                                                                              2.7.1.117) (MLCK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAD15922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD15922).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD15922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD15922,
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1914;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD15922
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAD15922,
                                                                                                                                                                                                                                              -KKLSKDRMKKYMARR
                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                            J.T.;
muscle
                                                                                             Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND
                                                                                                                                                                                                                               347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD15923
                             myosin light
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAD15923
                                                                                                                                                                                                                                                                                                                                                                                                               22;
                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                1688
                                                                                                                                                                                                                                                                                                                1628
                                                                                                                                                                                                                                                                                                                                               1570
                                                                                                                                                                                                                                                                                                                                                                                                65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AND
                                                                                                                                                                                                                                                 1743
                                                                                                                                                                                                                                                                                                244
                                                                                                                                                                                                                                                                303
                                                                                                                                                                                                                                                                                                                                                                                                                6
```

```
Pfam; PF00041; fn3; 1.

Pfam; PF00047; 19; 2.

Pfam; PF00069; Pk1nase; 1.

SMART; SM00060; FN3; 1.

SMART; SM00410; IG_11ke; 1.

SMART; SM00410; IG_21; 2.

SMART; SM00200; S_TKG; 1.

SMART; SM00220; S_TKG; 1.

SMART; SM00220; S_TKG; 1.

PROSITE; PS001107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00110; PROTEIN_KINASE_DOM; 1.

PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS0011; PROTEIN_KINASE_COM; 1.

PROSITE; PS0011; PROTEIN_KINASE_COM; 1.

PROSITE; PS0011; PROTEIN_KINASE_COM; 1.

PROSITE; PS0011; PROTEIN_KINASE_COM; 1.
                                                                                                                                                                             CHAIN
INIT_MET
DOMAIN
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities
or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallagher P.J., Herring B.P.;
"The carboxyl terminus of the smooth muscle myosin light chain kinase is expressed as an independent protein, telokin.";
J. Biol. Chem. 266:23945-23952(1991).
-1-FUNCTION: PHOSPHORYLATES A SPECIFIC SERINE IN THE N-TERMINUS OF A
                                                                                           REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY ALTERNATIVE INITIATION, A NON-MUSCLE FORM (WHICH IS THE LO FORM); A SMOOTH-MUSCLE FORM AND TELOKIN (A C-TERMINAL SECTION NO CATALYTIC ACTUITY).

-I- DOMAIN: TELOKIN BINDS CALMODULIN.
-I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
-I- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
-I- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
           REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M76233; AAA73093.1; -. EMBL; M76234; AAA31408.1; -. EMBL; M76181; AAA31409.1; -. PIR; A41675; A41675.
                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=92084695; PubMed=1748667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 993-1147 FROM N.A.
                                                                                                                                                                                                                                                                 Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MYOSIN LIGHT CHAIN.

CATALYTIC ACTIVITY: ATP + [myosin light-chain] - light-chain] phosphate.

ALTERNATIVE PRODUCTS: AT LEAST THREE ISOFORMS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P56276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s requires a license agreement (S an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                        IPR002290;
                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR003006;
IPR003598;
                                                                                                                                                                                                                                                                 initiation
1147
993
                                                                                                                                                       288
111
123
132
144
156
168
192
192
192
204
216
226
240
252
276
448
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Euk_pkinase.
FN_III.
Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                Ig_c2.
Ig_like.
                                                                                                                                                                                                                                                                                                                                                                                                                        Ser_thr_pkinase.
                                                                                                                                                                                                   TELOKIN.
FOR TELC
16 x 12
            MYOSIN LIGHT
FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                       ISOZYME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TELOKIN)
                                                                                                                                                                  (INCOMPLETE)
                                                                                                                                                                                                     X 12 AA TANDEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ST THREE ISOFORMS OF MLCK ARE PROL
NON-MUSCLE FORM (WHICH IS THE LON
AND TELOKIN (A C-TERMINAL SECTION
                                                                                                                                                                                                                  TELOKIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                    CHAIN KINASE, SMOOTH-MUSCLE
                                                                                                                                                                                                                                                                          domain;
                                                                                                                                                                                                                                                                                     Calmodulin-binding;
                                                                                                                                                                                                     REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [myosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E PRODUCED
HE LONGEST
CTION WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                its
```

```
Ş
                                                                                                                                                                                                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                                                                                                                                                                                                                                    õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
 뭐
                                                                                                                                                                                                                                                                                                                                                                                        Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
NP_BIND
BINDING
ACT_SITE
DOMAIN
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
DOMAIN
SEQUENCE OF 649-1906 FROM TISSUE=Fibroblast;
                                                           Olson N.J.,
Means A.R.;
                                                                                                                "Multiple gene products are produced from transcription region."; FEBS Lett. 373:217-220(1995).
                             Proc. Natl.
                                          "Regulatory and structural
chain kinase.";
                                                                                 SEQUENCE FROM N.A. (MLCK-108).
MEDLINE-90192792; PubMed-2315320;
                                                                                                                                               Watterson D.M., Collinge M., Lukas
Stepanova O.V., Shirinsky V.P.;
                                                                                                                                                                    SEQUENCE FROM N.A. (MLCK-210).
MEDLINE=96033976; PubMed=7589469;
                                                                                                                                                                                                   NCBI_TaxID=9031;
                                                                                                                                                                                                                         Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                           976
                                                                                                                                                                                                                                                                                                                                                                                               304
                                                                                                                                                                                                                                                                                                                                                                                                                  921
                                                                                                                                                                                                                                                                                                                                                                                                                                        245
                                                                                                                                                                                                                                                                                                                                                                                                                                                            861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 QQKVEDFYDIGEELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVSREEIEREV 65
                                                                                                                                                                                                                                                                                                                                                                                     APEVINYEPISYATDMWSIGVICYILVSGLSPFMGDNDNETLANVTSATWDFDDEAFDEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APEIVNYEPLGLEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSYDFDEEFFSHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DGVNYLHTKKIAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGTPEFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GIMNCLHHPKLVQCVDAFEEKANIVMVLEIVSGGELFERIIDEDFELTERECIKYMRQIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SILRQVLHHNVITLHDVYENRTDVVHILELVSGGELFDFLAQKE-SLSEEEATSFIKQIL 124
                                                                                                                                                                                                                                                                                                                                                                           KWQKTGNAVRAIGRLSSMAMISGLSGRKSSTGSPTSPLTAERLETEEDVSQ
                                                                                                                                                                                                                                                                                                                                                                                                                  SDDAKDFISNLLKKDMKNRLDCTQCLQHPWLMKDTKNMEA-----KKLSKDRMKKYMARR
                                                                                                                                                                                                                                                                                                                                                                                                                                      SELAKDFIRKLLVKETRKRLTIQEALRHPWI-TPVDNQQAMVRRESVVNLENFRKQYVRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGVEYIHKQGIVHLDLKPENIMCVNKT--GTRIKLIDFGLARRLENAGSLKVLFGTPEFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EQKVSDFYDIEERLGSGKFGQVFRLVEKKTGKIWAGKFFKAYSAK-----EKENIPAEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146;
                                         kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               696
943
1056
702
725
725
1138
1114
                               Acad.
                                                                       Pearson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             951
1006
1123
710
725
725
817
1147
                               Sci. U.S.A.
                                                                     R.B.,
                                                                                                                                                                                                                        Chordata; Craniata; Vertebrata; Euteleostomi;
Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125719
                                                                       Needleman D.S.,
         Ν.Α.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEIN KINASE.
CALMODULIN-BINDING.
IG-LIKE C2-TYPE DOMAIN.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
POLY-GLU.
C -> R (IN REF. 2).
IS MW; F039E624C6E31024 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63;
                                                   motifs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 694; DB 1;
Pred. No. 6.5e-35;
                               87:2284-2288(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
         AND PARTIAL SEQUENCE
                                                   of
                                                                                                                                                          T.J.,
                                                   chicken
                                                                                                                                                         van
                                                                                                                                     a novel protein kinase
                                                                       Hurwitz M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120;
                                                                                                                                                          Eldik L.J.,
                                                 gizzard
                                                                                                                                                                                                                                                                  non-muscle isozymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                   myosin
                                                                        Kemp B.E.,
                                                                                                                                                                                                                                                                                                                                                                           1026
                                                                                                                                                           Birukov K.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184
                                                                                                                                                                                                                                                                                                                                                                                                                    975
                                                                                                                                                                                                                                                                                                                                                                                                                                                             920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5
```

```
DAN BERREAR BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Use of DNA sequence and mutant analyses and antisense oligodeoxynucleotides to examine the molecular basis of myosin light chain kinase autoinhibition, calmodulin reactivity":
                                                                                                                    EMBL; X52876; CAA37056.1; --
EMBL; X52876; CAA37057.1; --
EMBL; X52876; CAA37058.1; --
EMBL; X52876; CAA37059.1; --
EMBL; M31048; AAA49069.1; --
EMBL; M44953; AAA49083.1; --
EMBL; M96553; AAA49083.1; --
EMBL; M86283; AAA48647.1; --
EMBL; M86284; AAB53768.1; --
EMBL; EMBL; M86284; AAB53768.1; --
EMBL; M86284; AAB53768.1; --
EMBL; EMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-90361738; PubMed-2202734; Shoemaker M.O., Lau W., Shattuck R.L., Kwiatkowski Matrisian P.E., Guerra-Santos L., Wilson E., Lukas van Eldik L.J., Watterson D.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [6]
SEQUENCE OF 1750-1906 FROM N.A. (TELOKIN).
SEQUENCE OF 1750-1906 FROM N.A. (TELOKIN).
MEDLINE-92336611; PubMed-1373815;
Collinge M., Mattrislan P.E., Zimmer W.E., Shattuck R.L.
van Eldik L.J., Watterson D.M.;
van Eldik L.J., Watterson D.M.;
"Structure and expression of a calcium-binding protein
"Structure and expression of a calcium-binding protein
"Structure and expression of a calcium-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Guerriero V. Jr., Russo M.A., Olson N.J., Putkey J.A., Means A.R.; "Domain organization of chicken gizzard myosin light chain kinase deduced from a cloned cDNA,"; Biochemistry 25:8372-8381(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1259-1906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1750-1906 FROM N.A. (TELOKIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arch. Biochem. [6]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yoshikai S., Ikebe
"Molecular cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93073972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Gizzard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         within
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114ht-chain] phosphate.
114ht-chain] phosphate.
ALTERNATIVE PRODUCTS: AT LEAST THREE ISOFORMS OF MLCK ARE PRODUCED ALTERNATIVE INITIATION, A NON-MUSCLE FORM (MLCK-210; WHICH IS BY ALTERNATIVE INITIATION, A SMOOTH-MUSCLE FORM (MLCK-108) AND TELOKIN (A C-TERMINAL SECTION WITH NO CATALYTIC ACTIVITY).
C-TERMINAL SECTION WITH NO CATALYTIC ACTIVITY).
TISSUE SPECIFICITY: TELOKIN IS EXPRESSED IN GIZZARD, HEART, LUNG, TISSUE SPECIFICATY, AND SKELETAL MUSCLE ALTHOUGH THE LEVELS OF THE INVESTINE, AND SKELETAL MUSCLE MUSCLE THAN THAT IN THE GIZZARD.
EXPRESSION IN THE LATTER WERE MUCH LESS THAN THAT IN THE GIZZARD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hin a calmodulin-regulated protein kinase gene.;
Cell. Biol. 12:2359-2371(1992).
FUNCTION: PHOSPHORYLATES A SPECIFIC SERINE IN THE N-TERMINUS OF FUNCTION CHAIN, WHICH LEADS TO THE FORMATION CALMODULIN/MYOSIN LIGHT CHAIN, WHICH LEADS TO THE FORMATION CALMODULIN/MYOSIN LIGHT TANSDUCTION COMPLEXES WHICH ALLOW SELECTIVE TRANSDUCTION OF CALCIUM SIGNALS.
CATALYTIC ACTIVITY: ATP + [myosin light-chain] - ADP + [myosin CATALYTIC ACTIVITY: ATP + [myosin light-chain]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN: TELOKIN BINDS CALMODULIN.
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biol. 111:1107-1125(1990).
            IPR000719;
IPR003961;
IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biophys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=1444462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FROM
        ; Euk_pkinase.
; FN_III.
; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ne chicken gizzard telokin
299:242-247(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shattuck R.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of nonmuscle recognition,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lukas T.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and
```

```
20
                                                        Вþ
                                                                        Š
        Š
                         В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002290; Ser_thr.

Pfam; PF00041; fn3; 1.

Pfam; PF00047; fg; 9.

Pfam; PF00069; Pkinase; 1.

SMART; SM00400; FN3; 1.

SMART; SM00410; IG_1ke; 1.

SMART; SM00400; IG_2; 8.

SMART; SM00400; S_TKC; 1.

SMART; SM00220; S_TKC; 1.
                                                                                                  Query Match
Best Local
                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
INIT_MET
INIT_MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transferase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transferase; Serine/threonine-protein_kinase;
                                                                                                                                                                                                                                                                                                                                                                           BINDING
                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      interPro;
                                                                                                                                 REPEAT
DOMAIN
DOMAIN
MOD_RES
MOD_RES
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                  REPEAT
REPEAT
                                                                                                                                                                                                                                                                          REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                   DOMAIN
REPEAT
                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alternative initiation
                                                                                                                                                                                         REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                         REPEAT
REPEAT
                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                            REPEAT
                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                          1446
                                                                                                                                                                                                                  DOMAIN
                         1500
                                         66
                                                                                                   Local Similarity
                                                                         6 QQKVEDFYDIGEELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVSREEIEREV
                                                          EQKVSDVYNIEERLGSGKFGQVFRLVEKKIGKVWAGKFFKAYSAK-----EKENIRDEI 1499
DGVNYLHTKKIAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGTPEFV
                         SILRQVLHHNVITLHDVYENRTDVVHILELVSGGELFDFLAQKE-SLSEEEATSFIKQIL 124
                                                                                           140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR003600;
IPR002290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR003598;
                                                                                                                                                                                                                                                                                                                                                                                                             1750
935
1750
1330
                                                                                                                                                          1140
1281
1851
970
970
999
1061
1209
1700
1896
                                                                                                                                                                                                                                                                           1107
1817
                                                                                                                                                                                                                                                                                                                                                                                      1459
                                                                                                                                                                                                                                                                                                                                                                                                                                                      935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phosphorylation;
                                                                                            Conservative
                                                                                                                                    ÀA;
                                                                                                                                                                                                                                                                                                                                                                                     1906
935
1750
1400
1708
1708
1876
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1906
                                                                                                                                                                                                                                                                                            1364
1402
1833
676
774
                                                                                                                                                                                                                                                                                                                                              1749
                                                                                                                                                                                                                                                                            1123
1833
                                                                                                                                                                                                                                                           1866
708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig_c2.
Ig_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ser_thr_pkinase
                                                                                                    37.18;
                                                                                                                                     210445
                                                                                            58;
                                                                                                                                     ΜŒ;
                                                                                                                                                                                                                                                                                                                                                                                                                                              MYOSIN LIGHT CHAIN KINASE, SMOOTH-MUSCLE ISOZYME (MLCK-108).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MYOSIN LIGHT CHAIN KINASE, NON-MUSCLE
                                                                                                                                                                                                                                                                                                                                                                               PROTEIN KINASE.
IG-LIKE C2-TYPE DOMAIN.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                       FOR MLCK-108.
                                                                                                                                                                                                                                                              IIA-4
5 X R
IIB-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ISOZYME (MLCK-210)
                                                                                                                                                                                                                                                                                                     I-VI
                                                                                                                                                                                                                                                                                                                                               CALMODULIN RECOGNITION
                                                                                                                                                                                                                                                                                                                                                             CALMODULIN AUTOINHIBITION (AM13) REGION
                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                FIBRONECTIN TYPE-III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunoglobulin domain;
                                                                                                                                                                                                                    IIB-5
                                                                                                                                                                                                                                             IIB-2
IIB-3
                                                                                                                                                                                                                                                                                                              4 X REPEATS,
                                                                                                                                                                                                                                                                                                                       MOTIF IB
                                                                                            Score 685.5; DB 1
Pred. No. 3.8e-34;
B; Mismatches 107
                                                                                                                                    PHOSPHORYLATION.
PHOSPHORYLATION.
R -> Q (IN REF. 4).
W; AD7D8A3B69EB3363 CRC64;
                                                                                                                                                                      CALMODULIN-BINDING POLY-GLU.
                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                       POTENTIAL).
                                                                                                                                                                                                                                                                      REPEATS,
                                                                                                                                                                                                                     REPEATS, MOTIF III.
                                                                                                                                                                                                                                                                                                                MOTIF
                                                                                                                                                                                                                                                                       MOTIF IIB
                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Calmodulin-binding;
                                                                                                                                                                                                                                                                                                                 IIA
                                                                                                            Length
                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                (RS20) REGION
                                                                                                               1906;
                                                                                                 15;
                                                                                                 Gaps
                184
                                                                                                  ú
```

```
RESULT 6
SIJA_H
SIJA_H
AC 109UEE5
DT 16-OCT
DT SUUC
CC EUkary
OC EUkary
OC Mammal
OC IN
RC JSJUE
RX MEDLIN
RC TISSUE
RX MEDLIN
RC INCHEL
CC -1- FI
CC -1- FI
CC -1- FI
CC -1- FI
CC Use E
CC Use TI
CC Use TI
CC Use TI
CC OT SET
CC Use TI
CC OT SET
CC OT SET
CC USE TI
CC OT SET
CC USE TI
CC OT SET
CC THEFT
DR INCHET
DR FROSIT
DR FROSIT
DR FROSIT
DR PROSIT
DR PROSIT
FT DOMAIL
FT DOMAIL
FT NP_BIL
FT DOMAIL
FT MUTAGI
SEQUEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
                      Phosphorylation;

DOMAIN 61

DOMAIN 33

NP_BIND 67

BINDING 90

MUTAGEN 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  $17A_HUMAN
Q9UEE5;
16-OCT-2001
                                                                                                                                                                                             InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 1.
SMART; SM00220; S_TKC; 1.
PROSTTE; PS00107; PROTEIN_KINASE_ATP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Serine/threonine kinase 17A (EC 2.7.1..) (DAP
appoptosis-inducing protein kinase 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1560
                                                                                                                                                        PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein kinase that trigger apoptosis.";
J. Biol. Chem. 273:29066-29071(1998).
I- FUNCTION: PHOSPHORYLATES THE MYOSIN LIGHT CHAIN (MLC) AS AN EXOGENOUS SUBSTRATE AND IS INVOLVED IN APOPTOTIC SIGNALING. THE TERMINAL REGION PLAYS AN IMPORTANT ROLE IN KINASE ACTIVITY AND F INITIATION OF APOTOSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Placenta, and Liver; MEDLINE-99003259; PubMed-9786912;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STK17A OR DRAK1
      SEQUENCE
                                                                                                                                          Transferase;
                                                                                                                                                                                                                                                                                                  MIM; 604726;
                                                                                                                                                                                                                                                                                                                                       EMBL; AB011420; BAA34126.1;
                                                                                                                                                                                                                                                                                                                                                                               or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sanjo H., Kawai T., Akira S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "DRAKS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Nuclear.
TISSUE SPECIFICITY: HIGHLY EXPRESSED
LEVELS IN HEART, LUNG, SKELETAL MUSCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTM: AUTOPHOSPHORYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KWQKTGHAVRAIGRLSSMAM 1752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SELAKDFIRKLLVKETRKRLTIQEALRHPWI-TPVDNQQAMVRRESVVNLENFRKQYVRR 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APEVINYEPIGYETDMWSIGVICYILVSGLSPFMGDNDNETLANVTSATWDFDDEAFDEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APEIVNYEPLGLEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSYDFDEEFFSHT 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RWKLSFSIVSLCNHLTRSLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDDAKDFISNLLKKDMKSRLNCTQCLQHPWLQKDTKNMEA----KKLSKDRMKKYMARR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGVEYIHKQGIVHLDLKPENIMCVNKT--GTSIKLIDFGLARRLESAGSLKVLFGTPEFV 1617
                                                                                                                                                                                                                                                                                                                                                                               an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     novel serine/threonine kinases related
                                                                                                                                                                                                                                                                                                                                                                           squires a license agreement (See http://www.isb-sib.ch/announce/
email to license@isb-sib.ch).
                                                                                                                                        Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                                                                                       1PHK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                       Nuclear
                        321
37
75
90
      46559
                                                                                                 protein; Apoptosis
PROTEIN KINASE
      ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          323
POLY-PRO.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
K->A: LOSS OF ACTIVITY.
K->A: CC140290438C2A1A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ESSED IN PLACENTA AND IN LOWER MUSCLE, KIDNEY AND PANCREAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LYS-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         kinase-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ដ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     death-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FOR C-
```

```
В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
S17A_RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                      STKI/A ON MARANA.
ORYCTOLAGUS CUNICULUS (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota: Phrheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOHN C. (1981) (Rel. 40, Creaceu, 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 16-OCT-2001 (Rel. 40, Last annotation update) Serine/threonine kinase 174 (EC 2.7.1.-) (DAP kinase-related serine/threoning protein kinase 1) (rDRAK1).
                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                             EMBL; AB042195; BAB16111.1; ... InterPro; IPR000719; Euk_pkinase. InterPro; IPR002290; Ser_thr_pkinase. InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                          TISSUE-Osteoclast;
MEDLINE-21276420; PubMed-11279167;
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9GM70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S17A_RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     341 N-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 EPFKQQKVEDFYDI--GEELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVS-R 58
                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES
                                                                                                                                                                                                                TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LEVELS IN BRAIN, HEART, LUNG, LIVER AND PTM: AUTOPHOSPHORYLATED (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REIMGTPEYVAPEILSYDPISMATDMWSIGVLTYVMLTGISPFLGNDKQETFLNISQMNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DVQRLMRQILEGVHFLHTRDVVHLDLKPQNILLTSES-PLGDIKIVDFGLSRILKNSEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEITHETAVL-ELAQDNPWVINLHEVYETASEMILVLEYAAGGETFDQCVADREEAFKEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NFRKQYVRRRWKLSFSIVSLCNHLTRSLMKKVHLRPDEDLRNCESDTEEDIARRKAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DFDEEFFSHTSELAKDFIRKLLVKETRKRLTIQEALRHPWITPVDNQQAMVRRESVVNLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KNIFGTPEFVAPEIVNYEPLGLEADMWSIGVITVILLSGASPFLGDTKQETLANITSVSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EATSFIKQILDGVNYLHTKKIAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEF: ::||::||::||::::|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SYSEEEFDVLSESAVDFIRTLLVKKPEDRATAEECLKHPWLTQSSIQEPSFRMEKALEEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EEIEREVSILRQVLHHN--VITLHDVYENRTDVVHILELVSGGELFD--FLAQKESLSEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EPF----QDGYSLCPGRELGRGKFAVVRKCIKKDSGKEFAAKFMRKR-----RKGQDCR 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----ALQEGHSVPEINSDTDKSETEESIVTEELI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 668.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A
                                                                                                                                                                                                                                    KIDNEY
                                                                                                                                                                                                                                                BONE MARROW AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95;
                                                                                                                                                                                                                                                                                                                                         M., Liu Y strongly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                          Liu Y.-K.;
                                                                                                                                                                                                                                                                                               (BY
                                                                                                                                                                                                                                                                                                                                            expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45;
                                                                                                                                                                                                                                                  Ä
                                                                                                                                                                                                                                                  LOWER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           220
```

```
R PEAM; PE00069; pkinase; 1

R SMART; SM00219; TYTKC; 1

OR SMART; SM00219; TYTKC; 1

PROSITE; PS00107; PROTEIN_KINASE_ST; 1

DR PROSITE; PS00118; PROTEIN_KINASE_DOM; 1

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1

R PROSITE; PS50011; PROTEIN_KINASE_DOM; 1

R PROSITE; PS50011; PROTEIN_KINASE, ATP-binding; Phosphorylation; Nuclear protein; Apoptosis.

KW Phosphorylation; Nuclear PROTEIN KINASE.

RW PHOSPHORY AND SMILLARITY).

SO ATP (BY SIMILARITY).

Tength in the protein in the prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DR DR DR DR DR DR DR KW KW FT FT FT SQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Вb
SITE_HUMAN
ID S17E_H
AC 094768
AC 094768
DT 16-0CT
DT 16-0CT
DT 16-CCT
CC CC -1-
CC CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            덩
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  094768;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Est annotation update)
Serine/information of the control of the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         204
                                                                                                                                                                                                           Sanjo H., Kawai T., Akira S.;
"DRAKG, novel serine/threonine kinases related to death-associated "DRAKG, novel serine/threonine kinases related to death-associated protein kinase that trigger apoptosis.";
protein kinase that trigger apoptosis.";
J. Biol. Chem. 273:29066-29071(1998),
J. BIOL. Chem. 273:29066-29071(1998),
J. FUNCTION: PHOSPHORYLANTES THE MYOSIN LIGHT CHAIN (MLC) AS AN EXCENOUS SUBSTRATE AND IS INVOLVED IN APOPTOTIC SIGNALING. THE EXOGENOUS SUBSTRATE AND IS INVOLVED IN KINASE ACTIVITY AND TERMINAL REGION PLAYS AN IMPORTANT ROLE IN KINASE ACTIVITY AND TERMINAL REGION PLAYS AN IMPORTANT ROLE IN KINASE ACTIVITY AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND MUTAGENESIS TISSUE-Placenta, and Liver; MEDLINE-99003259; PubMed-9786912;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 apoptosis-inducing protein STK17B OR DRAK2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EPF----ODCVSLSPGRELGRGKFAVVRKCIOKDSGKEFAAKEMRKR-----RKGQDCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EPFKQQKVEDFYDI--GEELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVS-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EEIEREVSILROVLHHN--VITLHDVYENRTDVVHILELVSGGELFD--FLAQKESLSEE 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYSEEEFDTVSESAVDFIKKLLVKKPEDRATAEECLKHPWLTQSSIQDPVLRVKEALEEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EATSFIKQILDGVNYLHTKKIAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEDEEFESHTSELAKDEIRKLLVKETRKRLTIQEALRHPWITPVDNQQAMVRRESVVNLE 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HUMAN
                                              INITIATION OF APOTOSIS.
SUBCELLULAR LOCATION: Nuclear.
TISSUE SPECIFICITY: HIGHLY EXP
AND IN LOWER LEVELS IN HEART,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 43.5
31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 659.5;
Pred. No. 2.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                          EXPRESSED RT, BRAIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     372 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .3e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LYS-62
                                                                              IN PLACENTA, LUNG,
LIVER, SKELETAL MU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              kinase-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19;
                                                                                                 MUSCLE
                                                                                                          PANCREAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85
                                                                                                                                                                                                                                                                       THE C-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
```

```
SO TETE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q
                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                  ρ
                                                                                                                                                                                                                                                                                                                                                                                                 멍
                                                                                                                                                                                                                                                                                                                                                                                                                       QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                   g.
                                                                                                                                                                                                                                                                                                               δõ
                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                       δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 132
                                                                                                                                                                           RESULT
KMLS_SI
                                                                                                                                                                                                                                    밁
 OCCOS GERRARIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by an on-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pfam; pf00069; pkinase; 1.
prints; pr00109; TYRKINASE.
smart; SM00220; STYC; 1.
pr0SITE; ps00107; pr0TEIN_KINASE_ATP; 1.
pr0SITE; ps00108; pr0TEIN_KINASE_DM; 1.
pr0SITE; ps00101; pr0TEIN_KINASE_DM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phosphorylation; Nuclear protein; Apoptosis.

DOMAIN

DOMAIN

DOMAIN

NP_BIND

NP_BIND

NP_BIND

NP_BIND

NP_BIND

SEQUENCE

372

AA;

42344

MH;

Apportein; Apoptosis.

PROTEIN APOPTOSIS.

PROTEIN FINALAR

PROTEIN FINALAR

PROTEIN FINALAR

ATP (BY SIMILAR

K->A: LOSS OF AV

K->A: LOSS OF AV

K->A: LOSS OF AV

MT 7E69FFAED6DC11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transferase;
                                                                                002827;
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Myosin light chain kinase, smooth muscle (EC
Myosin light chain kinase, smooth).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTM: AUTOPHOSPHORYLATED. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES
                                                                                                                                                                                SHEEP
Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pec
Boyldae; Caprinae; Ovis.
NCBI_TaxID-9940;
                                                                                                                                                                   KMLS_SHEEP
                                                                                                                                                                                                                                                                                                                                              137
                                                                                                                                                                                                                                                                                           196
                                                                                                                                                                                                                                                                                                                                                                                                                                                     238
                                                                                                                                                                                                                                     256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 PFKQQKVEDFYDI-GEELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVS-REE
                                                                                                                                                                                                                                                                                                                                                                                                                          IEREVSILROVLH-HNVITLHDVYENRTDVVHILELVSGGELFDFLAOK--ESLSEEEAT
                                                                                                                                                                                                                                                                                                                                             SFIKQILDGVNYLHTKKIAHEDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNI 177
                                                                                                                                                                                                                                                                                                                                                                                                 ILHEIAVLELAKSCPRVINLHEVYENTSEIILILEVAAGGEIFSLCLPELAEMVSENDVI 136
                                                                                                                                                                                                                                                                                        132;
                                                                                                                                                                                                                                    EEFFSHTSELAKDFIRKLLVKETRKRLTIQEALRHPWITPVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UULL: PROTEIN_KINASE_DOM; 1.
Serine/threonine-protein kinase;
                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 641.5; DB 1
pred. No. 2.7e-32;
49; Mismatches 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLY-SER.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
K->A: LOSS OF ACTIVITY.
7E69FFAED6DC1FF3 CRC64;
                                                                                                                                                                             PRT;
                                                                                                                                                                             438
                                                                                                                                                                             B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATP-binding;
                                                                                                             2.7.1.117)
                                                                                                                                                                                                                                                                             279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                          Pecora;
                                                        Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        372;
                                                                                                                (MLCK)
                                             Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60
                                                                                                                                                                                                                                                                                                              255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6;
```

```
Ş
 В
                    Ś
                                               멍
                                                                   Š
                                                                                                밁
                                                                                                                                               В
                                                                                                                                                                     Ş
                                                                                                                                                                                             밁
                                                                                                                                                                                                                   á
                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 133
                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00408; IGc2; 1.
SMART; SM00220; S_TKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; PARTIAL.
PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transferase; Serine/threonine-protein_kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for nomentities requires a lineage account.
                                                                                                                                                                                                                                                                                                               DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 myosin light chain kinase.";
Mol. Cell. Biochem. 149:59-65(1995).
-1- FUNCTION: PHOSPHORYLATES A SPECIFIC SERINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003598; Ig_c2.
InterPro; IPR002290; Ser_th
Pfam; PF00047; Ig; 1.
Pfam; PF00069; Pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=96139839; PubMed=8569750;
Pato M.D., Kerc E., Lye S.J.;
Phosphorylation and partial sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                            ATP-binding; Phosphorylation; Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MYOSIN LIGHT CHAIN.
-1- CATALYTIC ACTIVITY: ATP + [myosin light-chain] -
                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                  119
                                                                                                                         151
                                                                                                                                                                          92
                                                                                                                                                                                                                         32
                                                                                                                                                                                                  G
                                              NIPIPHIKLIDFGLAHEIEDGVEFKNIFGTPEFVAPEIVNYEPLGLEADMWSIGVITYIL
QHPWLXXXTKNMEA-----KKLSKHRMKKYMARRKWQKTGNAVRAIGRLSSMAMISGLSG
                       RHPWI-TPVDNQQAMVRRESVVNLENFRKQYVRRRWKLSFSIVSLCNHLTRSLM-----
                                                                                                T--GTRIKLIDFGLARRLENAGSLKVLFGTPEFVAPEVINYEPIGYATDMWSIGVICYIL
                                                                                                                                                             ILELVSGGELFDFLAQKE-SLSEBEATSFIKQILDGVNYLHTKKIAHFDLKPENIMLLDK
                                                                                                                                                                                                EKKTGKVWAGKFFKAYSAK-----EKENIRQEISIMNCLHHPKLVQCVDAFEEKANIVM
                                                                                                                                                                                                                      EKSTGLEYAAKFIKKROSRASRRGVSREEIEREVSILROVLHHNVITLHDVYENRTDVVH
                                                                                                                                               VLEIVSGGELFERIIDEDFELTERECIKYMKQISEGVEYIHKQGIVHLDLKPENIMCVNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S80867; AAB50715.2; -. P56276; ITLK.
                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR000719; Euk_pkinase
                                                                                                                                                                                                                                                                                                             <1
233
346
15
107
107
283
433
                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                               438
49503
                                                                                                                                                                                                                                                                                                                                       241
296
413
15
107
                                                                                                                                                                                                                                                            34.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ser_thr_pkinase
                                                                                                                                                                                                                                                                                                               ¥.
                                                                                                                                                                                                                                                  61;
                                                                                                                                                                                                                                               Score 637; DB Pred. No. 6.1e 61; Mismatches
                                                                                                                                                                                                                                                                                                                                               PROTEIN KINASE.
CALMODULIN-BINDING.
IG-LIKE C2-TYPE DOMAIN.
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                            POLY-GLU.
77A02F4885A10B51 CRC64;
                                                                                                                                                                                                                                                                                                                                       TELOKIN
                                                                                                                                                                                                                                                              .1e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pregnant sheep
                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                            domain
                                                                                                                                                                                                                                                                                                                                                                                                                                      Calmodulin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IN THE
                                                                                                                                                                                                                                                                        Length 438;
                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-TERMINUS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        myometrium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           + [myosin
                                                                                                                                                                                                                                                 22;
                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     commercial
                                                                                                176
                                                                                                                                                118
                                                                                                                                                                       150
                                                                                                                                                                                                58
                                                                                                                                                                                                                        91
                        323
                                                                        270
                                                                                                                       210
                                               236
                                                                                                                                                                                                                                                 6;
```

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                    EMBL; J05194; AAA31400.1; -.
PIR; A25830; A25830.
PIR; A05120; A05120.
PIR; A35021; A35021.
PDB; 2BBM; 31-JAN-94.
PDB; 2BBM; 31-JAN-94.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR000719; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RMIC_RABIT STANDARD; PRT; 607 AA.

PO7313;
01-APR-1988 (Rel. 07, Created)
01-APR-1990 (Rel. 14, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Myosin light chain kinase, skeletal muscle (EC 2.7.1.117) (MICK).

POTYCTOLAGUS CUNICULUS (Rabbit).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RABIT
                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-87101105; PubMed-3542042;
Takio K., Blumenthal D.K., Walsh K.A., Titani K., Kreb "Amino acid sequence of rabbit skeletal muscle myosin kinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                    multidimensional NMR.";
Science 256:632-638(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Amino acid sequence of an active myosin light chain kinase."; Biochemistry 24:6028-6037(1985).
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                           Pfam; PF00069; pkinase; SMART; SM00220; S_TKC;
                                                                                                                                                                                                                                                                                                                                                                   -1- FUNCTION: PHOSPHORYLATES A SPECIFIC SERINE IN THE MYOSIN LIGHT CHAIN.
-1- CATALYTIC ACTIVITY: ATP + [myosin light-chain] -
                                                                                                                                                                                                                                                                                                                                                                                                                                               Ikura M., Clore G.M., Gro
"Solution structure of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=92263094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRUCTURE BY NMR OF 577-602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ritani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Takio K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-86104095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 295-603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochemistry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-603.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Herring B.P., Stull J.T., "Domain characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=90110242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biol. Chem. 265:1724-1730(1990).
                                                                                                                                                                                                                                                                                                                                 light-chain) phosphate.
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RKSSTGSPTSPLNAEKLESEEDVSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -KKVHLRPDEDLRNCESDTEEDIAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6104095; PubMed=3841288; Blumenthal D.K., Edelma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25:8049-8057(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=1688558;
ll J.T., Gallagher P.J.;
ization of rabbit skelet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=1585175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gronenborn
                                                                                                                                                                                                                                                                                                                                                                                                                                                 onenborn A.M., Zhu G., Klee C.B., calmodulin-target peptide complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Edelman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fragment of rabbit skeletal muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.M., Walsh K.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            skeletal
                                                                                                                                                                                                                                                                                                                                                                                                    SERINE IN THE N-TERMINUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           muscle myosin light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Krebs
                                                                                                                                                                                                                                                                                                                                                                                                                                                   complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Krebs
                                                                                                                                                                                                                                                                                                                                                                        ADP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bax
by
                                                                                                                                                                                                                                                                                                                                                                      (myosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Α.,
                                                                                                                                                                                                                                                                                                                                                                                                        얶
                                                                                                                                                                                                                                                                                                                                                                                                    ×
```

```
SO STATE OF THE ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δÃ
B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δÕ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Sim
Matches 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INIT_MET
MOD_RES
DOMAIN
DOMAIN
NP_BIND
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TURN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transferase;
ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 p20689;
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Myosin light chain kinase, skeletal muscle (EC
Rattus norvegicus (Rat).
                                                                                                                                   ROUSH C.L., Kennelly P.J., Glaccum M.B., Helfman D.M. Krebs E.G.;
"Isolation of the cDNA encoding rat skeletal muscle m chain kinase. Sequence and tissue distribution.";
J. Biol. Chem. 263:10510-10516(1988).
-I. FUNCTION: PHOSPHORYLATES A SPECIFIC SERINE IN THE MYOSIN LIGHT CHAIN.
-I. CATALYTIC ACTIVITY: ATP + [myosin light-chain] -
                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELIX
                                                                                                                                                                                                                                                                                                MEDLINE-88273159; PubMed-2839493; MEDLINE-88273159; PubMed-2839493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KMLC_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300
  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                            light-chain] phosphate.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVSREEIEREVSILRQVLHHNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EALGGGKFGAVCTCTEKSTGLKLAAKVIKKQTPK-----DKEMVMLEIEVMNQLNHRNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LCNHLTR 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IVKEQGARMSAAQCLAHPWLNNLAEKAKRCNRRLKSQILL---KKYLMKRRWKKNFIAVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LVKETRKRLTIQEALRHDWITPVDNQQAMVRR--ESVVNLENFRKQYVRRRWKLSFSIVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSYDFDEEFFSHTSELAKDFIRKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LHLDLKPENILCVNTTGHL--VKIIDFGLARRYNPNEKLKVNFGTPEFLSPEVVNYDQIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGTPEFVAPEIVNYEPLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IQLYAAIETPHEIVLEMEYIEGGELFERIVDEDYHLTEVDTMVFVRQICDGILFMHKMRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ITLHDVYENRTDVVHILELVSGGELFDFLAQKE-SLSEEBATSFIKQILDGVNYLHTKKI 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AANRFKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  296
585
302
325
325
417
417
335
581
596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Serine/threonine-protein kinase; Calmodulin Phosphorylation; Acetylation; 3D-structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACETYLATION.

PROTEIN KINASE.

CALMODULIN-BINDING.

ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.

BY SIMILARITY.

K -> KK (IN REF. 2 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 605; DB 1;
Pred. No. 7.7e-30;
                                                                                                                                                                                            A SPECIFIC SERINE IN THE N-TERMINUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6E677641751A04C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KK (IN REF. 2 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    609
                                                                                                                                                                                                                                                                                                                 Helfman D.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ã
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Calmodulin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 607;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.7.1.117) (MLCK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ω
.
                                                                                                                                                                                                                                                                     myosin
                                                                                                                                                     ADP +
                                                                                                                                                                                                                                                                                                                   Scott J.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14;
                                                                                                                                                                                                                                                                       light
                                                                                                                                                  [myosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
```

```
SQUE TETT TO THE T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δÃ
KMLC_LDT
ID
ID
ID
KN
KN
KN
KN
AC
P2
AC
P3
AC
P4
AC
P4
AC
P5
AC
P6
AC
P7

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
NP_BIND
BINDING
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INIT_MES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transferase; Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; J03886; AAA41625.1;
PIR; A28798; A28798.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00069; pkinase; SMART; SM00220; S_TKC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000719; InterPro; IPR002290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transferase;
ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P00518; 1PHK
                                                                                                                                                                                                                                                                                                                                                                                                     P25323;
                                                                                                                                                                                                                                                                                  01-MAY-1992 (Rel. 22, Creat
01-OCT-1996 (Rel. 34, Last
16-OCT-2001 (Rel. 40, Last
Myosin light chain kinase (
                                                               SEQUENCE FROM N.A. STRAIN-AX3;
                                                                                                                                                  Eukaryota; Mycetozoa;
NCBI_TaxID=44689;
                                                                                                                                                                                                                                                  Myosin light MLKA.
      MEDLINE-91340753; PubMed=1651931; Tan J.L., Spudich J.A.;
                                                                                                                                                                                                                     Dictyostelium discoideum
                                                                                                                                                                                                                                                                                                                                                                                                                                        KMLC_DICDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DICDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGTPEFVAPEIVNYEPLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ITLHDYYENRTDVVHILELYSGGELFDFLAQKE-SLSEEEATSFIKQILDGVNYLHTKKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EALGGGKFGAVCTCTERSTGLKLAAKVIKKQTPK-----DKEMVLLEIEVMNQLNHRNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVSREEIEREVSILRQVLHHNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IQLYSAIETSHEIILFMEYIEGGELFERIVDEDYQLTEVDTMVFVRQICDGILFMHKMRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVKETRKRLTIQEALRHPWITPVDNQQAMVRR--ESVVNLENFRKQYVRRRWKLSFSIVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEADMWSIGVTTYILLSGASPFLGDTKQETLANITSVSYDFDEEFFSHTSELAKDFIRKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LHLDLKPENILCVNTTGHL--VKIIDFGLARRYNPNEKLKVNFGTPEFLSPEVVNYDQIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AANRFKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LCNHLTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ITKDQSARMSAEQCLAHPWLNNLAEKAKRCNRRLKSQILL---KKYLMKRRWKKNFIAVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              298
587
304
327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phosphorylation; Acetylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        553
599
312
327
419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ser_thr_pkinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Euk_pkinase.
                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
hase (EC 2.7.1.117) (MLC
                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                            pum (Slime mold)
Dictyosteliida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACETYLATION (BY SIMILARITY).
PROTEIN KINASE.
CALMODULIN-BINDING (BY SIMILAI
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 604; DB 1;
Pred. No. 8.9e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                 295
                                                                                                                                                                                                  Dictyostelium
                                                                                                                                                                                                                                                                                        (MLCK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Calmodulin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               commerc:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ņ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŭ
```

```
밁
                                                õ
                                                                                В
                                                                                                       Š
S
                                                                                                                                 몽
                                                                                                                                                          δ
                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                             Phosphorylation.

DOMAIN 8

DOMAIN 264

NP_BIND 14

BINDING 37

ACT_SITE 130

SEQUENCE 295 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spudich J. Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                      DictyDb; DD01034; mlkA.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A40811; A40811.
PIR; A37125; A37125.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Biol. Chem. 265:13818-138:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Characterization and bacterial expression of the Dictyostelium myosin light chain kinase cDNA. Identification of an autoinhibitory domain.";
                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1
                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00069; pkinase; SMART; SM00220; S_TKc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-90337997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-AX3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                            Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M64176; AAB06337.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Dictyostelium myosin light chain kinase. Purification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tan J.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spudich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REVISIONS
 187
                            118
                                                                                                           67
                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119ht-chain] phosphate.
ENZYME REGULATION: POSSESSES AN AUTOINHIBITORY DOMAIN.
ENZYME REGULATION: POSSESSES AN AUTOINHIBITORY DOMAIN.
AUTOPHOSPHORYLATION APPEARS TO INCREASE THE ENZYMATIC
DOES NOT HAVE A CALMODULIN-BINDING DOMAIN.
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MYOSIN LIGHT CHAIN.

CATALYTIC ACTIVITY: ATP + [myosin light-chain]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAMK SUBFAMILY.
                                           VNYLHTKKIAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGTPEFVAP 186
                                                                                                                                                          KVEDFYDIGEELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVSREE-IEREVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EM
EIVNYEPLGLEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSYDFDEEFFSHTSE 246
                                                                                              ILRQVLHHNVITLHDVYENRTDVVHILELVSGGELFDFLAQKESLSEEEATSFIKQILDG
                           VGYLHGLNIVHRDLKPENLLLKSKENHL-EVAIADFGLSKIIGQTLVMQTACGTPSYVAP
                                                                                                                                     EVEKIYEFKEELGRGAFSIVYLGENKQTKQRYAIKVINK-----SELGKDYEKNLKMEVD
                                                                                ILKKVNHPNIIALKELFDTPEKLYLVMELVTGGELFDKIVEKGSYSEADAANLVKKIVSA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   an email to license@isb-sib.ch).
                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AUG-1996)
                                                                                                                                                                                                                                                                                                                                                         Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1A06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              266:16044-16049(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          265:13818-13824(1990)
                                                                                                                                                                                                                                                                                                                                                                                                               S_TKC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=2380188;
                                                                                                                                                                                                                                                            265
295
22
37
130
130
33406 MW;
                                                                                                                                                                                                        29.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ូ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the
                                                                                                                                                                                           50;
                                                                                                                                                                                        Score 545.5;
Pred. No. 1.3e
50; Mismatches
                                                                                                                                                                                                                                                                         PROTEIN KINASE.
AUTOINHIBITORY DOMAIN.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Þ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIFIC SERINE
                                                                                                                                                                                                                                                            SIMILARITY.
546CAEED8F6ECD0B CRC64;
                                                                                                                                                                                                       No. 1.3e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN.
FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                       DВ
                                                                                                                                                                                             119;
                                                                                                                                                                                                                                                                                                                                                         ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ħ
                                                                                                                                                                                          Indels
                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THE N-TERMINUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  •
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADP
                                                                                                                                                                                                                     295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a collaboration
                                                                                                                                                                                          15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [myosin
                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ę
                                                                                                                                      57
                                                                                                                                                                66
                                                                                                                                                                                          5
```

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                   13
LRAT
                                                                                                                                                                                                                                            Ohnstede C.-A., Jenson K.F., Sahyoun N.;
Ca2+/calmodulin-dependent protein kinase enriched in
granule cells. Identification of a novel neuronal
calmodulin-dependent protein kinase.";
J. Biol. Chem. 264:5866-5875(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KCC4_RAT
P13234;
                                                                                                                                                                                                                                                                                                                                                                  "A novel Ca2+/calmodulin-dependent protein cell-specific calmodulin-binding protein ar gene.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ohmstede C.-A., Bland M.M., Merrill B.M., Sahyoun N.;
"Relationship of genes encoding Ca2+/calmodulin-dependent
kinase Gr and calspermin: a gene within a gene.";
Proc. Natl. Acad. Sci. U.S.A. 88:5784-5788(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND FAMALES, SEQUENCE FROM N.A., AND FAMALES, PubMed=1648230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1993 (Rel. 25, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Calclum/calmodulin-dependent protein kinase type IV catalytic chain
(EC 2.7.1.123) (CAM kinase-GR) (CAMK IV) [Contains: Calspermin].
                                                                                                                                                                                                                                                                                                       STRAIN-SPRAGUE-DAWLEY; TISSUE-Brain; MEDLINE-89174647; PubMed-2538431;
                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                               Means A.R., Cruzalegui
Slaughter G.R., Ono T.,
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE-91304387; PubMed-1649385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       289
                    SIMILARITY: BELONGS
                                         TISSUE SPECIFICITY:
TESTIS AND BRAIN.
                                                                                       CATALYTIC ACTIVITY: ATP + protein - ADP + O-phosphoprotein. ALTERNATIVE PRODUCTS: CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE
                                 PTM: THE N-TERMINAL
                                                                  SPLICING
                                                                           TYPE IV CATALYTIC
                                                                                                                                                                                                                                                                                                                                                     Cell. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOTKLVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LSFSIVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EAKDFIGKLLVVDVSKRLNATNALNHPWLKSNNSNNTI----DTVKM----KEYIVERQK 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAKDFIRKLLVKETRKRLTIQEALRHPWITPVDNQQAMVRRESVVNLENFRKQYVRRRWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OF 250-474 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                    11:3960-3971(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AND PARTIAL SEQUENCE
                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                        F)
                    OF CALSPERMIN IS BLOCKED TO THE SER/THR FAMILY OF
                                                       CALSPERMIN
                                                                                                                                                                                                                                                                                                                                                                                                          Lemagueresse
                                                                            AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata;
Sciurognathi; Muridae,
                                                                            CALSPERMIN
                                                       SI
                                                       PREDOMINANTLY
                                                                                                                                                                                                                                                                                                                                                                                                          B., Needleman D.
                                                                                                                                                                                                                                                                                                                                                                         are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A
                                                                                                                                                                                                                                                                                                                                                                                      kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                         derived
                                                                            OBTAINED
                      PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                      and
                                                                                                                        CALMODULIN-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Euteleostomi;
                                                      FOUND
                                                                                                                                                                                                                                                                                                                                                                          from
                                                                                                                                                                                                                                                                                                                                                                                     a male germ
                                                                                                                                                                                                                                                                                  cerebellar
                                                                            ВҮ
                                                                                                                                                                                                                                                                                                                                                                          the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
                                                      N
                                                                            ALTERNATIVE
                                                       MAMMALIAN
                                                                                                                                                                                                                                                                                                                                                                         same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               236
```

2.7.1.123)

```
SOLUTION OF THE STREET 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 γ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                           RESULT
KCC1_HU
                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M63334; AAA40865.1; -.
EMBL; M74488; AAA40845.1; ALT_SEQ.
EMBL; M64757; AAA40856.1; -.
EMBL; M64757; AAA40857.1; -.
EMBL; J04600; AAAA41867.1; -.
EMBL; J04446; AAA41867.1; -.
EMBL; J04446; AAA41867.1; -.
PIR; A41103; TVRTC4.
                                                                                                                                                                                                                                                Š
       SSSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Calmodulin-binding; 7
CCHAIN 306 47
CCHAIN 42 28
DOMAIN 42 28
NP_BIND 48 21
NP_BIND 71
ACT_SITE 160 11
DOMAIN 318 3
DOMAIN 393 3
DOMAIN 403 4
SEQUENCE 474 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00069; pkinase; SMART; SM00220; S_TKC; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00107; PROTEIN_KINASE_ATP
PROSITE; PS00108; PROTEIN_KINASE_ST;
PROSITE; PS50011; PROTEIN_KINASE_DOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interpro; IPR000719; Euk_pkinase
Interpro; IPR002290; Ser_thr_pkinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP;
KCC1_HUMAN
Q14012;
15-JUL-1998
15-JUL-1998
16-OCT-2001
                                                                                                                   HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125
                                                                                                                                                                                                                                                                                                   261
                                                                                                                                                                                                                                                                                                                                             240
                                                                                                                                                                                                                                                                                                                                                                                           203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34
                                                                                                                                                                                                           313
                                                                                                                                                                                                                                                       300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collaboration entry is copyright. It is produced through a collaboration entry is copyright. It is produced through a collaboration entry is copyright. It is produced through a collaboration entry is copyright. It is produced through a collaboration entry is copyright.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P00518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KOOKVEDFYDIGEELGSGOFAIVKKCREKSTGLEYAAKFIKKROSRASRRGVSREEIERE 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DGVNYLHTKKIAHFDLKPENIMLLDKNIPIPH--IKLIDFGLAHEIEDGVEFKNIFGTPE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VSILRQVLHHNVITLHDVYENRTDVVHILELVSGGELFDFLAQKESLSEEEATSFIKQIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KRDPLSDFFEVESELGRGATSIVYRCKQKGTQKPYALKVLKKT-----VDKKIVRTE
                                                                                                                                                                                                                                                                                                                                                                                                                                   FVAPEIVNYEPLGLEADMWSIGVITYILLSGASPFL---GDTKQETLANITSVSYDFDEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EAVAYLHENGIVHRDLKPENLLYA---TPAPDAPLKIADFGLSKIVEHQVLMKTVCGTPG
                                                                                                                                                                                                                                                                                                                                                                                           LQEFNARRKLKAAVKAVVASSRL
                                                                                                                                                                                                                                                  Y----VRRRWKLSFSIVSLCNHL 318
                                                                                                                                                                                                                                                                                                      FFSHTSELAKDFIRKLLVKETRKRLTIQEALRHPWITPVDNQQAMVRRESVVNLENFRKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Serine/threonine-protein kinase; ATP-binding; 
inding; Testis; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
            (Rel.
(Rel.
(Rel.
                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEIN_KINASE_ATP; 1.
            36,
40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euk_pkinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28.8%;
            Last sequence update)
Last annotation updat
                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
CALMODULIN-BINDING (POTENTIAL).
POLY-GLU.
POLY-GLU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CALSPERMIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -> M (IN REF. 2 F
56F71AC5644DED23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ed. No. 1.5e
Mismatches
                                                                                                         PRT;
                                                                                                         370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
.5e-25;
                                                                                                           B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 AND 4).
23 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85
                                                                                                                                                                                                                                                                                                                              312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
```

```
뫄
                                                                                         QY
                                                                                                                  В
                                                                                                                                    ρy
                                                                                                                                                                                                                            Ω
         Š
                              Бр
                                                                                                                                                            Query Match
Best Local S
Matches 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Edelman A.M., Snyderman R., Means A.R.;
Edelman A.M., Snyderman R., Means A.R.;
"Human calcium-calmodulin dependent protein kinase I: cDNA cloning, domain structure and activation by phosphorylation at threonine-177 by calcium-calmodulin dependent protein Kinase I kinase.";

BMBO J. 14:3679-3686(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Calcium/calmodulin-dependent protein kinase type I (EC CAM kinase I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nomo sapiens (numan).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                  NP_BIND
BINDING
ACT_SITE
MOD_RES
MUTAGEN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L41816; AAA99.
HSSP; Q63450; 1A06
                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase
                                                                                                                                                                                                                                                                                                                                                                                                       MIM; 604998;
           181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAMK SUBFAMILY.
                                                                                               63
                                                                                                                                REVSILROVLHHNVITLHDVYENRTDVVHILELVSGGELFDFLAQKESLSEEEATSFIKO
                                                                                                                    WKQAEDIRDIYDFRDVLGTGAFSEVILAEDKRTQKLVAIKCIAK-EALEGKEG----SME
PEFVAPETVNYEPLGLEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSYDFDEEF
                                                                         NEIAVLHKIKHENIVALDDIYESGGHLYLIMQLVSGGELFDRIVEKGFYTERDASRLIFQ
                                VLDAVKYLHDLGIVHRDLKPENLLYYSLDED---SKIMISDFGLSKMEDPGSVLSTACGT
                                                   ILDGVNYLHTKKIAHFDLKPENIML--LDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGT
                                                                                                                                                                          similarity
                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             AAA99458.1; -.
                                                                                                                                                                                                                      8
                                                                                                                                                                                                                        41337
                                                                                                                                                                            28.7%;
                                                                                                                                                                                                                         ¥.
                                                                                                                                                                                                                      ATP (BY SIMILARITY).

ATP BY SIMILARITY.

BY SIMILARITY.

PHOSPHORYLATION (AUTO-).

K->A: LOSS OF ACTIVITY.

K->A: LOSS OF ACTIVITY.

K->A: DOSS OF ACTIVITY.
                                                                                                                                                                    65;
                                                                                                                                                                            Score 530.5; DB 1;
Pred. No. 1.4e-25;
                                                                                                                                                                     Mismatches
                                                                                                                                                                       1.4e-25;
hes 126;
                                                                                                                                                                                             Length
                                                                                                                                                                           25;
                                                                                                                                                                           Gaps
                                                                                      124
                                                                                                             122
                                                                                                                                  64
                                                                                                                                                       62
                                              181
                                                                                                                                                                              ø
```

```
TERMENT TREE COMMENTS OF THE PRESCOND TO THE COMMENT OF THE PRESCOND TO THE PRESC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                뭐
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KCC1_RAT STANDARD; PRT; 374 AA. 063450; Q63084; 15-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) Calcium/calmodulin-dependent protein kinase type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-95035115; PubMed-7948038; Cho F.S., Phillips K.S., Bogucki B., Weaver "Characterization of a rat cDNA clone encodidependent protein kinase I.";
                                                                                                         EMBL; L24907; AAA19670.1; -.
EMBL; L26288; AAA66944.1; -.
PDB; 1A06; 08-Apr-98.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goldberg J., Nairn A.C., Kuriyan J.; "Structural basis for the autoinhibition of calclum/calmodulin-dependent protein kinase Cell 84:875-887(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutherla; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outsithe European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -I- FUNCTION: PHOSPHÓRYLATES SYNAPSIN I.
-I- CATALYTIC ACTIVITY: ATP + PROCEDIN = ADP + O-phosphoprotein.
-I- ENZYME REGULATION: ACTIVATED BY CA++-/CALMODULIN. MUST BE
-I- PHOSPHORYLATED TO BE MAXIMALLY ACTIVE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Picciotto M.R., Czernik A.J., Nairn A.C.;
"Calcium/calmodulin-dependent protein kinase I.
identification of autophosphorylation site.";
J. Biol. Chem. 268:26512-26521(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (37 KDA ISOFORM). MEDLINE-94075341; PubMed-8253780;
                                                         Pfam; PF00069; pkinase; 1.
SMART; SM00220; S_TKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochim. Biophys. Acta 1224:156-160(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (42 KDA ISOFORM).
STRAIN-SPRAGUE-DAWLEY; TISSUE-Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-96182648; PubMed-8601311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CAM kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: MONOMER.
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAMK SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KNFAKSKWKQAFNATAVVRH-----MRKLQLGTSQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KQYVRRRWKLSFSIVSLCNHLTRSLMKKVHLRPDED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGYVAPEVLAQKPYSKAVDCWSIGVIAYILLCGYPPFYDENDAKLFEQILKAEYEFDSPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WDDISDSAKDFIRHLMEKDPEKRFTCEQALQHPWIAGDTALDKN----IHQSV--SEQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FSHTSELAKDFIRKLLVKETRKRLTIQEALRHPWI---TPVDNQQAMVRRESVVNLENER 297
PS00107; PROTEIN_KINASE_ATP; 1. PS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; | Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OF SHORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         I. ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     calcium/calmodulin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     I (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Euteleostomi;
; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.7.1.123)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                    a collaboration -
                                                                                                                                                                                                                                                                                                                                                   for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and
                                                                                                                                                                                                                                                                                                                  .ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241
                                                                                                                                                                                                                                                                                                                                                                           no
                                                                                                                                                                                                                                                                                                                                                                                                            9
```

```
Š
                                                  뭐
                                                                           δÃ
                                                                                                        밁
                                                                                                                               Š
                                                                                                                                                           B
                                                                                                                                                                                   Ş
                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                      δÃ
                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                            Ş
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 120; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phosphorylation;
DOMAIN 20
DOMAIN 287
NP_BIND 26
BINDING 49
ACT_SITE 141
MOD_RES 177
VARSPLIC 323
                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50011;
                                                                                                        182
                                                                                                                                  181
                                                                                                                                                             125
296
                         298
                                                    242
                                                                             241
                                                                                                                                                                                      123
                                                                                                                                                                                                                 65
                                                                                                                                                                                                                                            63
                                                                                                                                                                                                                                                                     10
                                                                                                                                                                                                                                                                                            4 FKQ-QKVEDFYDIGEELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVSREEIE 62
KNFAKSKWKQAFNATAVVRH----MRKLQLGTSQE
                                                                                                                                PEFVAPEIVNYEPLGLEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSYDFDEEF 240
                                                                                                                                                                                                                 NEIAVLHKIKHPNIVALDDIYESGGHLYLIMQLVSGGELFDRIVEKGFYTERDASRLIFQ 124
                                                                                                                                                                                                                              REVSILRQVLHHNVITLHDVYENRTDVVHILELVSGGELFDFLAQKESLSEEEATSFIKQ 122
                                                                                                                                                                                                                                                                     WKQAEDIRDIYDFRDVLGTGAFSEVILAEDKRTQKLVAIKCIAKK-ALEGKEG----SME 64
                                                  WDDISDSAKDFIRHLMEKDPEKRFTCEQALQHPWIAGDTALDKN----IHQSV--SEQIK 295
                                                                            FSHTSELAKDFIRKLLVKETRKRLTIQEALRHPWI---TPVDNQQAMVRRESVVNLENFR
                                                                                                        PGYVAPEVLAQKPYSKAVDCWSIGVIAYILLCGYPPFYDENDAKLFEQILKAEYEFDSPY
                                                                                                                                                           VLDAVKYLHDLGIVHRDLKPENLLYYSLDED---SKIMISDFGLSKMEDPGSVLSTACGT
                                                                                                                                                                                     ILDGVNYLHTKKIAHFDLKPENIML--LDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGT 180
                        KQYVRRRWKLSFSIVSLCNHLTRSLMKKVHLRPDED
                                                                                                                                                                                                                                                                                                                                                                                         112
118
309
374
                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0011; PROTEIN KINASE DOM; 1. Serine/threonine-protein kinase; Calmodulin-binding; ion; ATP-binding; Alternative splicing; 3D-structure.
20 276 PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             276
321
34
49
141
177
                                                                                                                                                                                                                                                                                                                                                                                              41638
                                                                                                                                                                                                                                                                                                                                       28.7%;
35.7%;
                                                                                                                                                                                                                                                                                                                                                                                              ¥.
                                                                                                                                                                                                                                                                                                                           65;
                                                                                                                                                                                                                                                                                                                                                                                           F -> G (IN REF. 1).
A -> R (IN REF. 1).
A -> R (IN REF. 1).
A -> R (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                   ISOFORM).
F -> G (I
                                                                                                                                                                                                                                                                                                                                     Score 530.5; DB 1; Pred. No. 1.4e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHOSPHORYLATION (AUTO-).
TSQEGQGQTASHGELLTPTAGGPAAGCCCRDCCVEPGSELP
PAPPPSSRAMD -> HQPGGTGTDS (IN 37 KDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CALMODULIN-BINDING (BY ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY
                                                                                                                                                                                                                                                                                                                           Mismatches
                         333
                                                                                                                                                                                                                                                                                                                           126;
                                                                                                                                                                                                                                                                                                                                                                                              CRC64;
                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                     374;
                                                                                                                                                                                                                                                                                                                           25;
                                                                                                                                                                                                                                                                                                                        Gaps
                                                                             297
                                                                                                        241
                                                                                                                                                             181
```

9

Search completed: May 18, 2002, 05:12:35 Job time: 1436 sec